Figure 1A

```
   1  ATGACAACTCTTGTTCCTGCAACCCTCTCCTTCCTTCTTCTCTGGACCCTGCCAGGGCAG   60
   1  M  T  T  L  V  P  A  T  L  S  F  L  L  L  W  T  L  P  G  Q    20

  61  GTCCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGGTCCCAG  120
  21  V  L  L  R  V  A  L  A  K  E  E  V  K  S  G  T  K  G  S  Q    40

 121  CCCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCC  180
  41  P  M  S  P  S  D  F  L  D  K  L  M  G  R  T  S  G  Y  D  A    60

 181  AGGATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAAC  240
  61  R  I  R  P  N  F  K  G  P  P  V  N  V  T  C  N  I  F  I  N    80

 241  AGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA  300
  81  S  F  S  S  V  T  K  T  T  M  D  Y  R  V  N  V  F  L  R  Q   100

 301  CAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGAT  360
 101  Q  W  N  D  P  R  L  S  Y  R  E  Y  P  D  D  S  L  D  L  D   120

 361  CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAGGGGCC  420
 121  P  S  M  L  D  S  I  W  K  P  D  L  F  F  A  N  E  K  G  A   140

 421  AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTG  480
 141  N  F  H  E  V  T  T  D  N  K  L  L  R  I  F  K  N  G  N  V   160

 481  CTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCCTGATGGACCTCAAGAACTTCCCC  540
 161  L  Y  S  I  R  L  T  L  I  L  S  C  L  M  D  L  K  N  F  P   180

 541  ATGGACATCCAGACCTGCACGATGCAGCTTGAGAGCTTTGGCTACACCATGAAAGACCTC  600
 181  M  D  I  Q  T  C  T  M  Q  L  E  S  R  G  Y  T  M  K  D  L   200

 601  GTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGCCC  660
 201  V  F  E  W  L  E  D  A  P  A  V  Q  V  A  E  G  L  T  L  P   220

 661  CAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGG  720
 221  Q  F  I  L  R  D  E  K  D  L  G  C  C  T  K  H  Y  N  R  G   240

 721  AAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATT  780
 241  K  F  T  C  I  E  V  K  F  H  L  E  R  Q  M  G  Y  Y  L  I   260

 781  CAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATCAAC  840
 261  Q  M  Y  I  P  S  L  L  I  V  I  L  S  W  V  S  F  W  I  N   280

 841  ATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACC  900
 281  M  D  A  A  P  A  R  V  G  L  G  I  T  T  V  L  T  M  T  T   300
```

Figure 1B

```
901  CAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATC  960
301  Q  S  S  G  S  R  A  S  L  P  K  V  S  Y  V  K  A  I  D  I   320

961  TGGATGGCTGTGTGTCTGCTCTTTGTGTTCGCTGCCTTGCTGGAGTATGCTGCCATAAAT  1020
321  W  M  A  V  C  L  L  F  V  F  A  A  L  L  E  Y  A  A  I  N   340

1021 TTTGTTTCTCGTCAGCATAAAGAATTCATACGACTTCGAAGAAGGCAGAGGCGCCAACGC  1080
341  F  V  S  R  Q  H  K  E  F  I  R  L  R  R  R  Q  R  R  Q  R   360

1081 TTGGAGGAAGATATCATCCAAGAAAGTCGTTTCTATTTCCGTGGCTATGGCTTGGGCCAC  1140
361  L  E  E  D  I  I  Q  E  S  R  F  Y  F  R  G  Y  G  L  G  H   380

1141 TGCCTGCAGGCAAGAGATGGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCT  1200
381  C  L  Q  A  R  D  G  G  P  M  E  G  S  G  I  Y  S  P  Q  P   400

1201 CCAGCCCCTCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGACTGAGCCAAG  1260
401  P  A  P  L  L  R  E  G  E  T  T  R  K  L  Y  V  D             417

1261 AGAATTGACACCATCTCCCGGGCTGTCTTCCCTTTCACTTTCCTCATCTTCAATATCTTC  1320

1321 TACTGGGTTGTCTATAAAGTGCTACGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGG  1380

1381 TGGGAGCTATAGAGTCCTGCTGCTGGCCTCCTGCTTCCTCCTGGGTGGGCTTTCTCCCTC  1440

1441 AGTTAGACTCCATTAGGGGTTTGGACAGTTCCTTCCTGATCTCCCACTCAGAACTTCAAC  1500

1501 TACCAGTCCCAAAGCTATGTGGGCCTATATTGCATGGTGCCAATGGTGGCTGTACTTATA  1560

1561 AAGATGGCTTATCTACCCTAGTCCATATTTTCTCCATACTTTCCCATTTCTCATGAGACT  1620

1621 AAGGTTTGGCCACATTCCTGGGGCCAGGATGACCTTCTGCCCTTGCTGGAGCCTCCCTGT  1680

1681 TTTCCAATACTCCAGTGGAGAGTATTCAGAACACTGCTGCTAGATTCTGGCATTTGTCAT  1740

1741 CTTAATCTGCACCACTTCTCCCCCTGCCACCTCCCACCCAGAGCCTGGCCATTACTCTGT  1800

1801 CCTCTGTCCCTCCTGCTGCAGATTCAAATGGTGAGTTTCTCCTATCCACAAGTGCTGCCC  1860

1861 TGTGGGGCCTAGTCAGGTTTCCTTGAAGTGAGAGGAAGGCAAAGCCGCAAGTTCCCCACC  1920

1921 TCTCGAGAGGGTTGGAACAGTCATAGGCTGCACTGGGCTAGCGACTATATGGCCCAACAG  1980
```

Figure 1C

```
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2041  CTTGTCTGCTCTTTCCTGTTCACTGAGATACTCCTCTTGTCTGTCTCTTAGTTTTGAGGA  2100

2101  GAGCGTTCTGAGCTGACCAGGGTAGCTGGTTCAGAAATTACTGTCAGAATTGGGGCAGAG  2160

2161  ACTTTGGGTTCTCAAAAAGACTAACCTTCCAGATCCACCTGAACATTCTGGTCTCAGAAA  2220

2221  TATTCGTTCCGTTCCCTAATTAACTAGCATGGTGGCAGGATCTGTTGGACAGCTGGGGAG  2280

2281  TGTAAAAAAAGAAAAATACTTGTTCTTTAAGAAACTTACTTTATGATGCTAGAAAACTTT  2340

2341  TGAGAAAAGTGAGATCCAAGGTAGTGGAACCCAGGAGGAGTAGAATAGAGAAACTATTCT  2400

2401  CAGAGTGTCTTTTGTTGGCTGGGCTTTCATTTGTTTCTTCTTTCTCACCAAAGTCTATTT  2460

2461  TCCAGGGCCCTTCATTTCCAACCTGGTCTTTCACCTCCTTTTGGTGTGCAAATAAAGGTG  2520

2521  CCGCTGCAACCTTGTTAAGGATAAAAAAAAAAAAAAAAAAAAAAA  2565
```

Figure 2A

```
   1  ATGACAACTCTTGTTCCTGCAACCCTCTCCTTCCTTCTTCTCTGGACCCTGCCAGGGCAG   60
   1  M  T  T  L  V  P  A  T  L  S  F  L  L  L  W  T  L  P  G  Q    20

  61  GTCCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGGTCCCAG  120
  21  V  L  L  R  V  A  L  A  K  E  E  V  K  S  G  T  K  G  S  Q    40

 121  CCCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCC  180
  41  P  M  S  P  S  D  F  L  D  K  L  M  G  R  T  S  G  Y  D  A    60

 181  AGGATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAAC  240
  61  R  I  R  P  N  F  K  G  P  P  V  N  V  T  C  N  I  F  I  N    80

 241  AGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAA  300
  81  S  F  S  S  V  T  K  T  T  M  D  Y  R  V  N  V  F  L  R  Q   100

 301  CAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGAT  360
 101  Q  W  N  D  P  R  L  S  Y  R  E  Y  P  D  D  S  L  D  L  D   120

 361  CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAGGGGCC  420
 121  P  S  M  L  D  S  I  W  K  P  D  L  F  F  A  N  E  K  G  A   140

 421  AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTG  480
 141  N  F  H  E  V  T  T  D  N  K  L  L  R  I  F  K  N  G  N  V   160

 481  CTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCCTGATGGACCTCAAGAACTTCCCC  540
 161  L  Y  S  I  R  L  T  L  I  L  S  C  L  M  D  L  K  N  F  P   180

 541  ATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG  600
 181  M  D  I  Q  T  C  T  M  Q  L  E  S  S  S  I  L  C  S  P  L   200

 601  CCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTGAGTGGCTGGAA  660
 201  P  S  L  S  L  S  V  C  Y  T  M  K  D  L  V  F  E  W  L  E   220

 661  GATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGCCCCAGTTTATCTTGCGGGAT  720
 221  D  A  P  A  V  Q  V  A  E  G  L  T  L  P  Q  F  I  L  R  D   240

 721  GAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAATTCACCTGCATCGAG  780
 241  E  K  D  L  G  C  C  T  K  H  Y  N  T  G  K  F  T  C  I  E   260

 781  GTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGC  840
 261  V  K  F  H  L  E  R  Q  M  G  Y  Y  L  I  Q  M  Y  I  P  S   280

 841  CTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCTGCC  900
 281  L  L  I  V  I  L  S  W  V  S  F  W  I  N  M  D  A  A  P  A   300
```

Figure 2B

```
901  CGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCCGG  960
301  R  V  G  L  G  I  T  T  V  L  T  M  T  T  Q  S  S  G  S  R   320

961  GCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGTGTCTG  1020
321  A  S  L  P  K  V  S  Y  V  K  A  I  D  I  W  M  A  V  C  L   340

1021 CTCTTTGTGTTCGCTGCCTTGCTGGAGTATGCTGCCATAAATTTTGTTTCTCGTCAGCAT  1080
341  L  F  V  F  A  A  L  L  E  Y  A  A  I  N  F  V  S  R  Q  H   360

1081 AAAGAATTCATACGACTTCGAAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATC  1140
361  K  E  F  I  R  L  R  R  R  Q  R  R  Q  R  L  E  E  D  I  I   380

1141 CAAGAAAGTCGTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGAT  1200
381  Q  E  S  R  F  Y  F  R  G  Y  G  L  G  H  C  L  Q  A  R  D   400

1201 GGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCCTCTTCTAAGG  1260
401  G  G  P  M  E  G  S  G  I  Y  S  P  Q  P  P  A  P  L  L  R   420

1261 GAAGGAGAAACCACGCGGAAACTCTACGTGGACTGAGCCAAGAGAATTGACACCATCTCC  1320
421  E  G  E  T  T  R  K  L  Y  V  D                               431

1321 CGGGCTGTCTTCCCTTTCACTTTCCTCATCTTCAATATCTTCTACTGGGTTGTCTATAAA  1380

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1441 GCTGCTGGCCTCCTGCTTCCTCCTGGGTGGGCTTTCTCCCTCAGTTAGACTCCATTAGGG  1500

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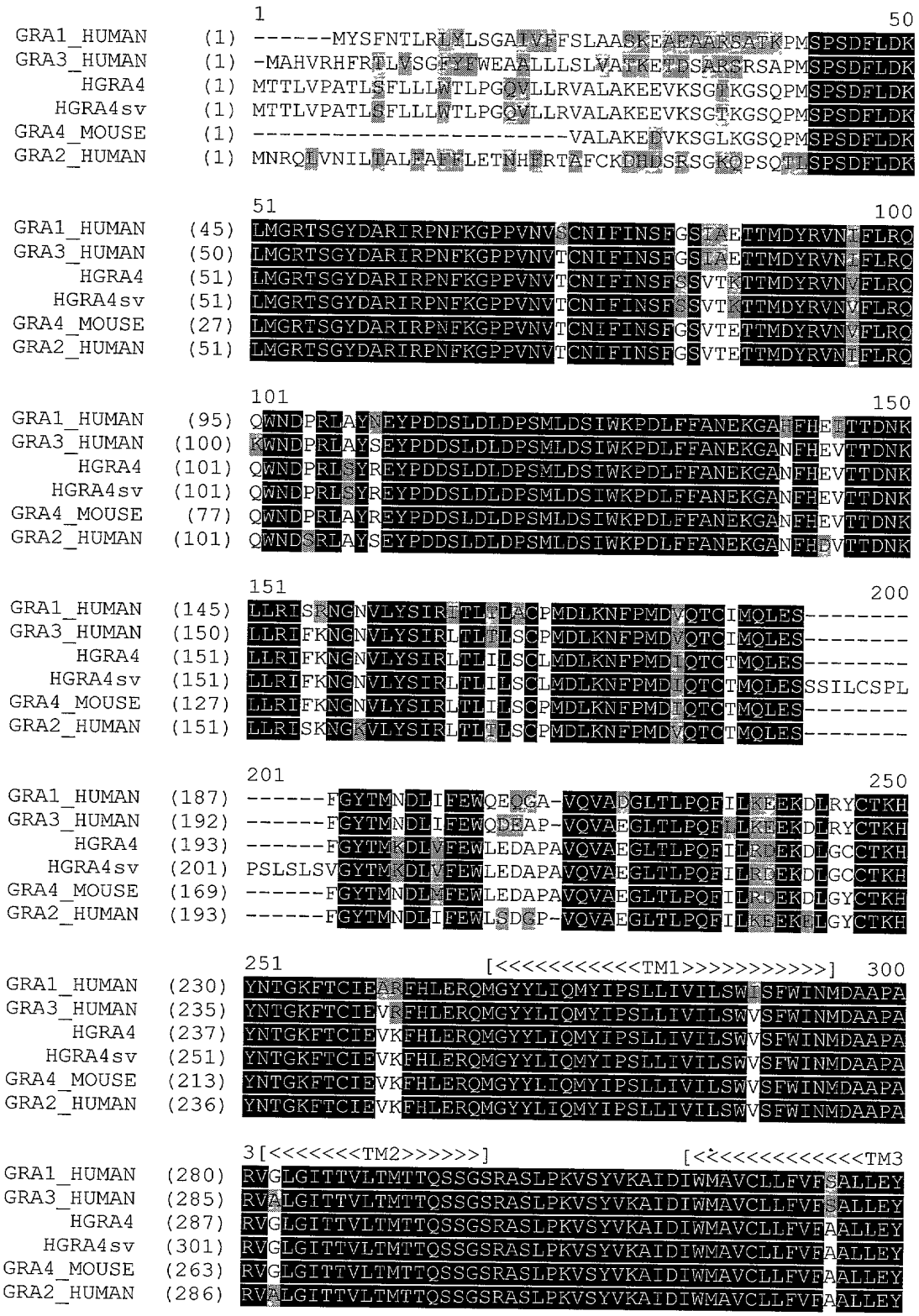
Figure 3A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HGRA4sv (1) MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDK
GRA4_MOUSE (1) ----------VALAKEDVKSGLKGSQPMSPSDFLDK
GRA2_HUMAN (1) MNRQLVNILIALFAFFLETNHFRTAFCKDHDSRSGKQPSQTLSPSDFLDK
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GRA1_HUMAN (45) LMGRTSGYDARIRPNFKGPPVNVSCNIFINSFGSIAETTMDYRVNTFLRQ
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GRA4_MOUSE (27) LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFGSVTETTMDYRVNVFLRQ
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GRA3_HUMAN (100) KWNDPRLAYSEYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNK
HGRA4 (101) QWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNK
HGRA4sv (101) QWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNK
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HGRA4 (287) RVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEY
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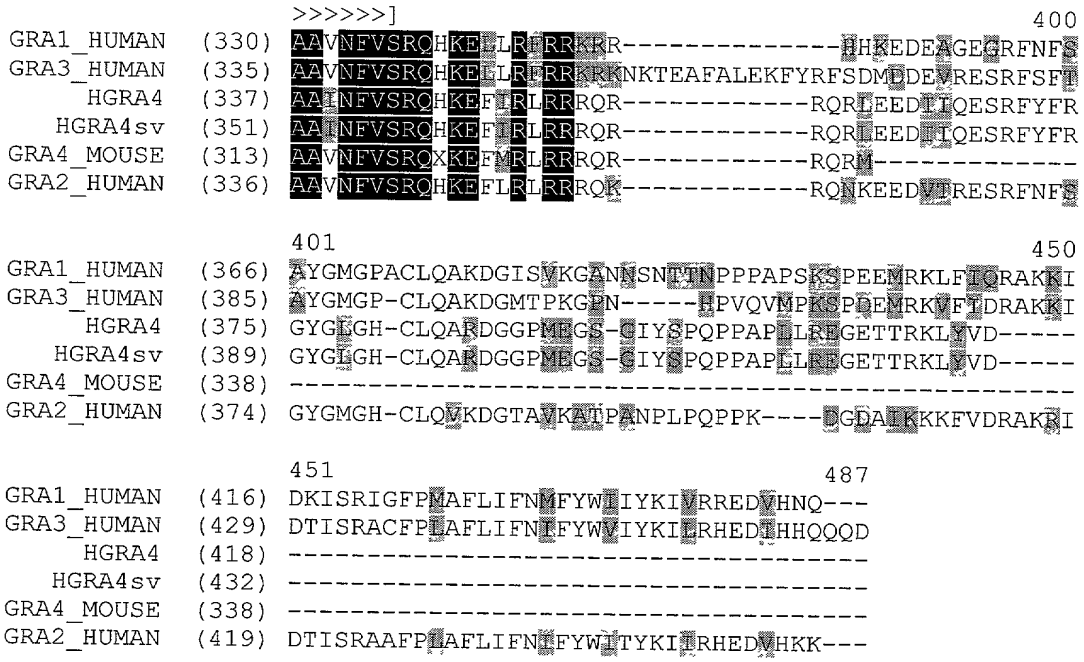
Figure 3B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HGRA4sv (351) AAINFVSRQHKEFIRLRRRQR----------RQRLEEDTIQESRFYFR
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GRA3_HUMAN (429) DTISRACFPLAFLIFNTFYWVIYKILRHEDTHHQQQD
HGRA4 (418) ----------
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Figure 4

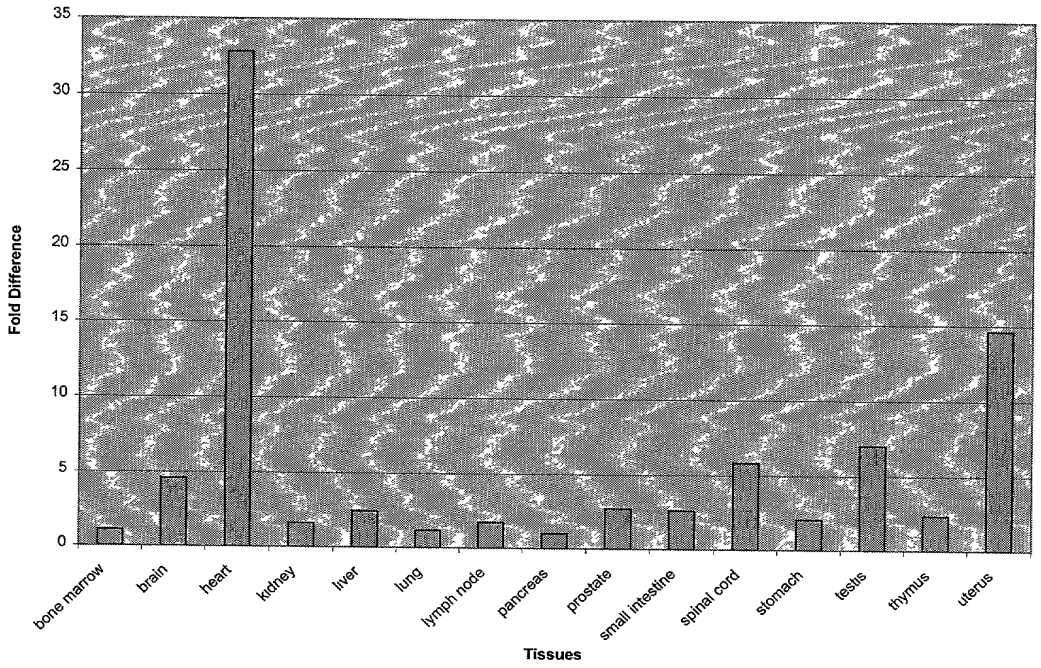
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Figure 5

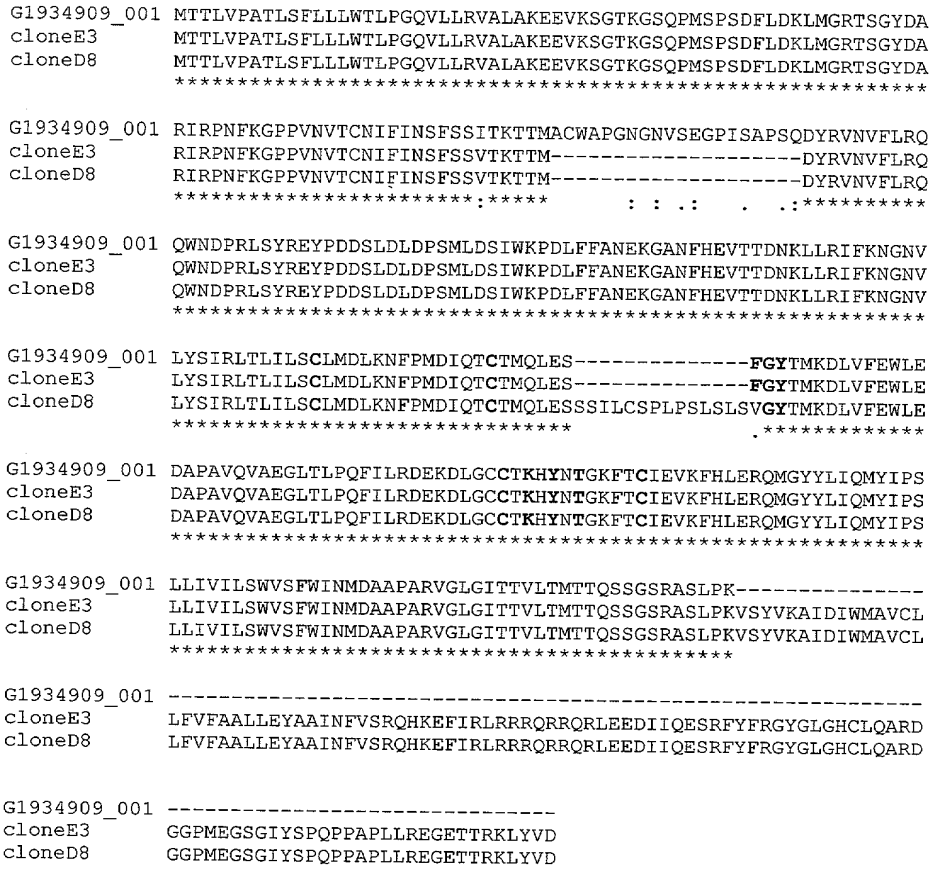
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Figure 6.

HGRA4

Protein	Genbank ID	Identities	Similarities
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human glycine receptor alpha 3 subunit	gi|5729844	84.4%	78.7%
mouse glycine receptor subunit alpha 4 protein	gi|817957	97%	96%
human glycine receptor alpha 2 subunit	gi|4504021	80.6%	86.5%

HGRA4sv

Protein	Genbank ID	Identities	Similarities
human glycine receptor alpha-1 subunit	gi|4504019	76.5%	82%
human glycine receptor alpha 3 subunit	gi|5729844	78.5%	84.2%
mouse glycine receptor subunit alpha 4 protein	gi|817957	95.8%	96.7%
human glycine receptor alpha 2 subunit	gi|4504021	80.3%	86.2%

Figure 7

Atgacaactcttgttcctgcaaccctctccttccttcttctctggaccctgccagggcaggtcctcctcagggtggcct
tggcaaaagaggaagtcaaatctggaaccaaggggtcccagcccatgtccccctctgatttcctagacaaacttatggg
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Figure 8

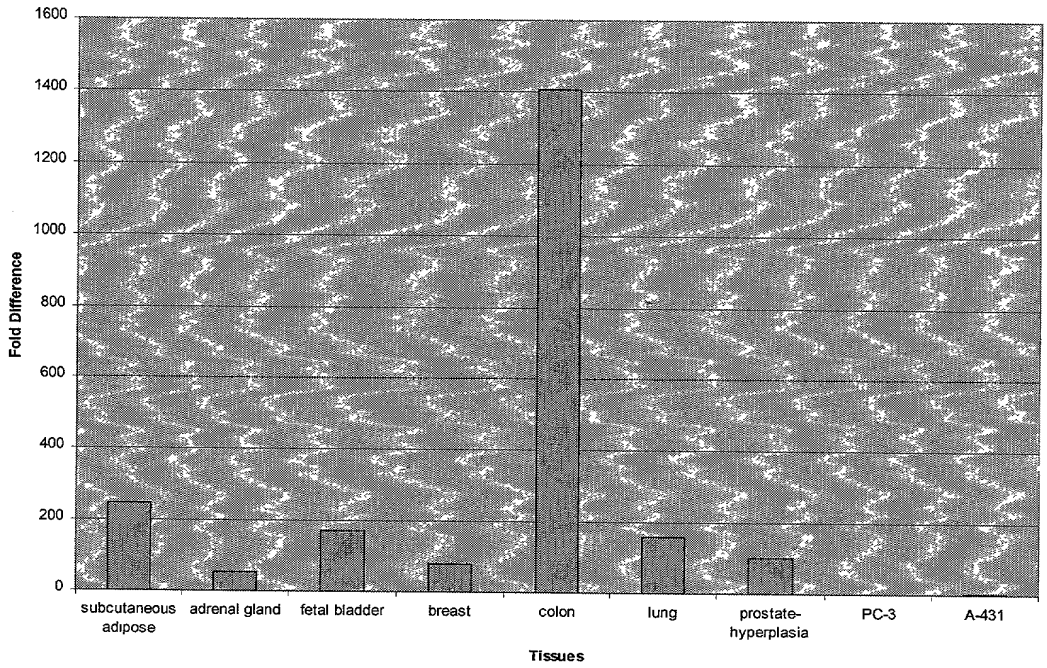
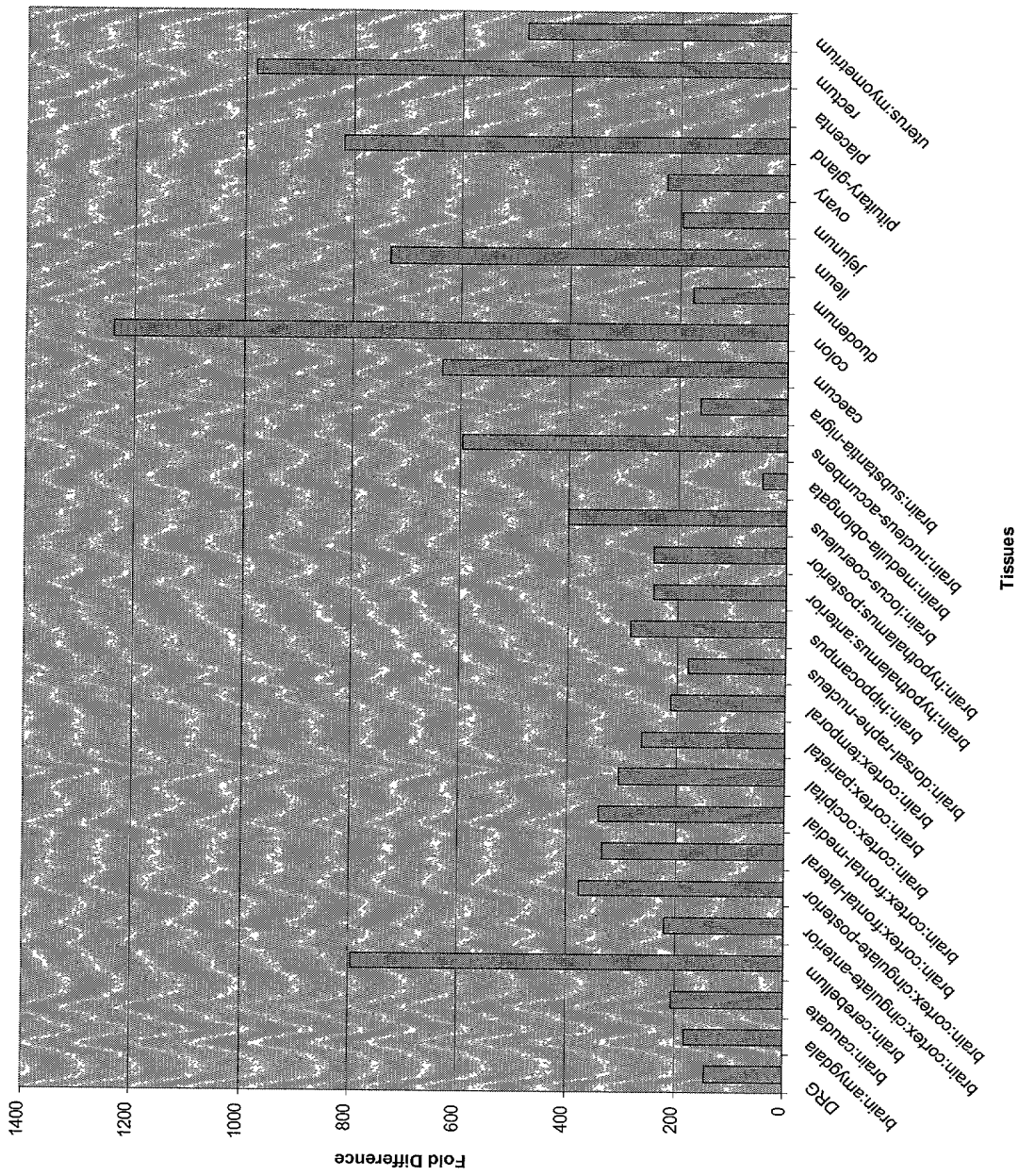

1600
1400
1200
1000
800
600
400
200
0
Fold Difference
subcutaneous adipose
adrenal gland
fetal bladder
breast
colon
lung
prostate-hyperplasia
PC-3
A-431
Tissues

Figure 9


Fold Difference
0
200
400
600
800
1000
1200
1400
DRG
brain:amygdala
brain:caudate
brain:cerebellum
brain:cortex:cingulate-anterior
brain:cortex:cingulate-posterior
brain:cortex:frontal-lateral
brain:cortex:frontal-medial
brain:cortex:occipital
brain:cortex:parietal
brain:cortex:temporal
brain:dorsal-raphe-nucleus
brain:hippocampus
brain:hypothalamus:anterior
brain:hypothalamus:posterior
brain:locus-coeruleus
brain:medulla-oblongata
brain:nucleus-accumbens
brain:substantia-nigra
caecum
colon
duodenum
ileum
jejunum
ovary
pituitary-gland
placenta
rectum
uterus:myometrium
Tissues